



PCT09

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,735

DATE: 10/23/2002
 TIME: 16:15:35

Input Set : A:\dorken.txt
 Output Set: N:\CRF4\10232002\I673735.raw

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3 <110> APPLICANT: DORKEN, Bernd
4     RIETHMULLER, Gert
5     KUFER, Peter
6     LUTTERBUSE, Ralf
7     BARGOU, Ralf
8     LOFFLER, Anja
10 <120> TITLE OF INVENTION: CD19XCD3 SPECIFIC POLYPEPTIDES AND USES THEREOF
12 <130> FILE REFERENCE: 028622/0102
14 <140> CURRENT APPLICATION NUMBER: US 09/673,735
15 <141> CURRENT FILING DATE: 2000-12-27
17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/02693
18 <151> PRIOR FILING DATE: 1999-04-21
20 <150> PRIOR APPLICATION NUMBER: EP 98107269.7
21 <151> PRIOR FILING DATE: 1998-04-21
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 36
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Primer
35 <400> SEQUENCE: 1
36 gaagcacgcg tagatattct gmtsacccaa wctcca 36
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42 <213> ORGANISM: Artificial Sequence
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48 gaagatggat ccagcgccg cagcatcagc 30
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52 <211> LENGTH: 33
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Primer
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63 <210> SEQ ID NO: 4
64 <211> LENGTH: 39
65 <212> TYPE: DNA

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66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Primer
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76 <211> LENGTH: 36
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Primer
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88 <211> LENGTH: 48
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Primer
95 <400> SEQUENCE: 6
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99 <210> SEQ ID NO: 7
100 <211> LENGTH: 48
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Primer
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114 <213> ORGANISM: Artificial Sequence
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117 <223> OTHER INFORMATION: Primer
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125 <212> TYPE: DNA
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130 <222> LOCATION: (11)..(1603)
131 <223> OTHER INFORMATION:
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135 gaattccacc atg gga tgg agc tgt atc atc etc ttc ttg gta gca aca      49
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139	gct	aca	ggt	gtc	cac	tcc	gac	tac	aaa	gat	gat	gac	gat	aag	gat	atc	97
140	Ala	Thr	Gly	Val	His	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Asp	Ile	
141	15					20				25							
143	cag	ctg	acc	cag	tct	cca	gct	tct	ttg	gct	gtg	tct	cta	ggg	cag	agg	145
144	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	
145	30				35					40				45			
147	gcc	acc	atc	tcc	tgc	aag	gcc	agc	caa	agt	ggt	gat	tat	gat	ggt	gat	193
148	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	
149				50					55					60			
151	agt	tat	ttg	aac	tgg	tac	caa	cag	att	cca	gga	cag	cca	ccc	aaa	ctc	241
152	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro	Lys	Leu	
153				65					70					75			
155	ctc	atc	tat	gat	gca	tcc	aat	cta	ggt	tct	ggg	atc	cca	ccc	agg	ttt	289
156	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser	Gly	Ile	Pro	Pro	Arg	Phe	
157			80					85				90					
159	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	aac	atc	cat	cct	gtg	337
160	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	
161	95					100					105						
163	gag	aag	gtg	gat	gct	gca	acc	tat	cac	tgt	cag	caa	agt	act	gag	gat	385
164	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys	Gln	Gln	Ser	Thr	Glu	Asp	
165	110				115						120				125		
167	ccg	tgg	acg	ttc	ggg	gga	ggg	acc	aag	ctc	gag	atc	aaa	ggg	ggg	ggg	433
168	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	
169				130					135					140			
171	ggg	tct	ggc	ggc	ggc	ggc	tcc	ggg	ggg	ggg	ggg	tct	cag	gtg	cag	ctg	481
172	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
173				145					150					155			
175	cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	tcc	tca	gtg	aag	att	529
176	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ser	Ser	Val	Lys	Ile	
177				160					165					170			
179	tcc	tgc	aag	gct	tct	ggc	tat	gca	ttc	agt	agc	tac	tgg	atg	aac	tgg	577
180	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser	Ser	Tyr	Trp	Met	Asn	Trp	
181	175					180						185					
183	gtg	aag	cag	agg	cct	gga	cag	ggg	ctt	gag	tgg	att	gga	cag	att	tgg	625
184	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Gln	Ile	Trp	
185	190				195					200					205		
187	cct	gga	gat	ggg	gat	act	aac	tac	aat	gga	aag	ttc	aag	ggg	aaa	gcc	673
188	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	
189				210					215					220			
191	act	ctg	act	gca	gac	gaa	tcc	tcc	agc	aca	gcc	tac	atg	caa	ctc	agc	721
192	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	
193				225					230					235			
195	agc	cta	gca	tct	gag	gac	tct	gcg	gtc	tat	ttc	tgt	gca	aga	cgg	gag	769
196	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Glu	
197				240				245					250				
199	act	acg	acg	gta	ggc	cgt	tat	tac	tat	gct	atg	gac	tac	tgg	ggc	caa	817
200	Thr	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	
201				255			260					265					
203	ggg	acc	acg	gtc	acc	gtc	tcc	tcc	gga	ggg	ggg	gga	tcc	gat	atc	aaa	865

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204	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	
205	270					275					280					285	
207	ctg	cag	cag	tca	ggg	gct	gaa	ctg	gca	aga	cct	ggg	gcc	tca	gtg	aag	913
208	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	
209					290					295						300	
211	atg	tcc	tgc	aag	act	tct	ggc	tac	acc	ttt	act	agg	tac	acg	atg	cac	961
212	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	
213					305					310						315	
215	tgg	gta	aaa	cag	agg	cct	gga	cag	ggt	ctg	gaa	tgg	att	gga	tac	att	1009
216	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	
217					320					325						330	
219	aat	cct	agc	cgt	ggt	tat	act	aat	tac	aat	cag	aag	ttc	aag	gac	aag	1057
220	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	
221					335					340						345	
223	gcc	aca	ttg	act	aca	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	caa	ctg	1105
224	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	
225	350					355					360					365	
227	agc	agc	ctg	aca	tct	gag	gac	tct	gca	gtc	tat	tac	tgt	gca	aga	tat	1153
228	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	
229					370					375						380	
231	tat	gat	gat	cat	tac	tgc	ctt	gac	tac	tgg	ggc	caa	ggc	acc	act	ctc	1201
232	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	
233					385					390						395	
235	aca	gtc	tcc	tca	gtc	gaa	ggt	gga	agt	gga	ggt	tct	ggt	gga	agt	gga	1249
236	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	
237					400					405						410	
239	ggt	tca	ggt	gga	gtc	gac	gac	att	cag	ctg	acc	cag	tct	cca	gca	atc	1297
240	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	
241					415					420						425	
243	atg	tct	gca	tct	cca	ggg	gag	aag	gtc	acc	atg	acc	tgc	aga	gcc	agt	1345
244	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	
245	430					435					440					445	
247	tca	agt	gta	agt	tac	atg	aac	tgg	tac	cag	cag	aag	tca	ggc	acc	tcc	1393
248	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	
249					450					455						460	
251	ccc	aaa	aga	tgg	att	tat	gac	aca	tcc	aaa	gtg	gct	tct	gga	gtc	cct	1441
252	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	
253					465					470						475	
255	tat	cgc	ttc	agt	ggc	agt	ggg	tct	ggg	acc	tca	tac	tct	ctc	aca	atc	1489
256	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	
257					480					485						490	
259	agc	agc	atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	caa	cag	tgg	1537
260	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	
261					495					500						505	
263	agt	agt	aac	ccg	ctc	acg	ttc	ggt	gct	ggg	acc	aag	ctg	gag	ctg	aaa	1585
264	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
265	510					515					520					525	
267	cat	cat	cac	cat	cat	cat	tagtcgac										1611
268	His	His	His	His	His	His											

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269                      530
272 <210> SEQ ID NO: 10
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274 <212> TYPE: PRT
275 <213> ORGANISM: Homo sapiens
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283 Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile Gln Leu Thr
284                      20                      25                      30
287 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
288                      35                      40                      45
291 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
292                      50                      55                      60
295 Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
296 65                      70                      75                      80
299 Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
300                      85                      90                      95
303 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
304                      100                     105                     110
307 Asp Ala Ala Thr Tyr His Cys Gln Ser Thr Glu Asp Pro Trp Thr
308                      115                     120                     125
311 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
312                      130                     135                     140
315 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
316 145                     150                     155                     160
319 Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
320                      165                     170                     175
323 Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
324                      180                     185                     190
327 Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
328                      195                     200                     205
331 Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
332                      210                     215                     220
335 Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
336 225                     230                     235                     240
339 Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
340                      245                     250                     255
343 Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
344                      260                     265                     270
347 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln
348                      275                     280                     285
351 Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys
352                      290                     295                     300
355 Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys
356 305                     310                     315                     320
359 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
360                      325                     330                     335
363 Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu

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VERIFICATION SUMMARY

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